

Figure 1

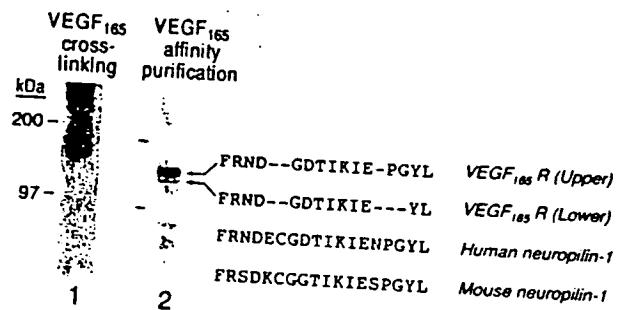


Figure 2A



Figure 2B



03580803-053000

Figure 3

1 MERGLPLLCAVLALVLA~~PAGA~~FRNDKCGDTIKIESPGYL~~TSPGYPHSYHPSEKCEWL~~IQAPDPYQRIMIN 70  
71 FNPHFDLEDRCKYDYVEVFDGENENGHFRGKFCGRIAPPPVVSSGPFLFIRKFVSDYETHGAGFSIRYEI 140  
141 FKRGPECSQNYTTPSGVIRSPGFPEKYPNSLECTTIVFAPKMSEIILEFESFOLEPDSNPPGMFCRYDR 210  
211 LEIWDGFPDVPHIGRCGQKTPGRIRSSSGILSHMVFYTD~~SAIAKEGFSANYSVLQSSVSEDFKCM~~EA~~LG~~ 280  
281 MESGEIHSDQITASSQY~~STNWSAERSRLN~~Y~~PENGWTPGEDSYREWIQV~~DLG~~LLRFVTAVGTQGAIS~~KETK 350  
351 K~~YV~~YV~~KTY~~KIDV~~SSNGEDW~~TIKEGNKPVL~~FQGNTNPT~~OVVVAVFPKPLITRFVRIKPA~~T~~WTGISM~~R~~FE 420  
421 VY~~GCK~~ITD~~YPCSGMLGMV~~SGLIS~~DSQITSSNQ~~CDRN~~W~~MPENIRLV~~TSRSGWALPPA~~PHSY~~Y~~IN~~E~~WLQ~~IDLG~~ 490  
491 ZEKIVRG~~II~~IQGGKHRENKV~~FMRKF~~KIGYSNN~~GS~~DW~~KM~~IM~~DDSKR~~KAKS~~FEGNN~~NYDTP~~E~~LRTFP~~ALSTR~~ 560  
561 F~~IRI~~YPERATHGGLGLRMELLGCEVEAPTAGPTTPNGNLV~~DECODDQ~~ANCHSGT~~GDDF~~QLTGGTTV~~LATE~~ 630  
631 KPTVIDSTIQSEFPTYGFNCEFGNGSHKTFCHWEHDNHVQLKWSVLT~~S~~KT~~G~~PIQDHTG~~D~~G~~N~~FIYSQADEN 700  
701 Q~~KGK~~V~~ARL~~V~~SPVVY~~SQMSAHC~~MT~~EWYHMSGSHV~~G~~T~~L~~R~~V~~K~~R~~YQ~~K~~PE~~Y~~D~~Q~~L~~V~~W~~H~~A~~I~~G~~H~~Q~~G~~D~~H~~W~~E~~GRV~~V~~LL 770  
771 HKSLKLYQV~~IF~~EGEIGKGNLGGIAV~~DD~~ISIN~~H~~ISQ~~ED~~CA~~K~~PA~~D~~L~~DK~~K~~N~~PE~~I~~K~~I~~DET~~G~~ST~~P~~GY~~E~~GE~~E~~GD 840  
841 KNISRKPGNVLK~~TLD~~PI~~L~~IT~~II~~AMSALGV~~LL~~GA~~V~~CGV~~V~~LYC~~A~~CHNGM~~SERN~~L~~SA~~EN~~Y~~N~~F~~EL~~V~~D~~G~~V~~KL~~ 910  
911 KD~~KL~~NTQ~~STY~~SEA 923

06580803 - 0633000

Figure 4

Comparative Deduced Amino Acid Sequences of Human VEGF<sub>165</sub>R/NP and VEGF<sub>165</sub>R/NP-1

VEGF <sub>165</sub> R/NP-2	1	MDMF-PGTH-VFLALYFSRHRQVRGQPDP?CGG-RLN SK--DA-----GY	50
VEGF <sub>165</sub> R/NP-1		MERGLPPLLCAV-LAL-----VLA-PA---GAER-NDKCGDTIKIESPGY	
NP-2	51	ITSPGY?PQDY-PSHQNCZW-IVYAPEPNQKIVLNENP?PFEIEKHDCRYDF	100
NP-1		LTSPGY?PNSYHPSEK-CEWLIQ-APD?YQRMIMNFN?P?F?D?C?D?C?YD?	
NP-2	101	IIZIRDGOSESADLLGKHCNIAAPP?I?SSGSMLYIKFTSD?YAR?GAG?E?I	150
NP-1		VEVF?D?G?E?N?E?N?G?H?E?R?G?I?C?G?K?I?A?P?P?V?V?S?G?P?F?L?I?K?F?V?S?D?Y?E?T?H?G?A?G?E?I?	
NP-2	151	RYZIFK?TG?S?D?C?S?K?N?F?T?P?N?G?T?I?E?S?P?G?P?E?K?Y?P?H?N? -LDCTFTIL-AKP?K?M?	200
NP-1		RYZIFK?R?G?P?E? -CSQNYTTPSGV?I?K?S?P?G?P?E?K?Y?P? -NSLECTY-I?V?F?A? -P?K?M?	
NP-2	201	-E?I?L?Q?F?L?F?D?L?E?H?D? - - - - - P?L?Q?V?G?E?G?D? - C?K?Y?D?W?L?D?I?W?D?G?I?P?H?V?G?P?L?I?G?K?Y?C?G?	250
NP-1		SE?I?I?L?E?F?E?S?P?D?L?E?P?D?S?N?P?P? - - - - - G? - G?M?F?C?R?Y?D?R?L?E?I?W?D?G?I?P?D?V?G?P?H?I?G?Y?C?G?	
NP-2	251	T?K?T?P?S?E?L?R?S?S?T?G?I?L?S?L?T?F?H?T?D?M?A?V?A?K?G?E?S?A?R?Y?Y?L?V?H?Q?E?P?L? - E?N?F?Q?C?N?V?P?	300
NP-1		Q?K?T?P?G?R?I?R?S?S?G?I?L?S?M?V?Y?T?D?S?A?I?A?K?E?G?F?S?A?Y?S? - V?L?Q?S?S?V?S?D?F?K?C?M?E?	
NP-2	301	L?G?M?E?S?G?R?I?A?N?E?Q?I?S?A?S?S?T?Y?S?D?G?R?W?T?P?Q?Q?S?R?L?H?G?D?D?N?G?W?T?P?N?L?D?S?N?K?E?Y?I?Q?	350
NP-1		L?G?M?E?S?G?E?I?H?S?D?Q?I?T?A?S?S?Q?Y?S?T?N? - W?S?A?E?R?S?R?L?N?Y?P?E?N?G?W?T?P?G?E?D?S?Y?R?E?W?I?Q?	
NP-2	351	V?D?L? - - - R?E?L?T?M?L?T?A? - - - A?T?Q?G?A?I?S?R?E?T?Q?N?G?Y?Y?V?R?S?Y?K?L?E?V?S?T?H?G?E?D?W?M?V?Y?R?H?	400
NP-1		V?D?L?G?L?L?R?F?V?T? - - - A?V?G?T?Q?G?A?I?S?K?E?T?K?K?Y?Y?V?K?T?Y?K?I?D?V?S?S?N?G?E?D?W?I?T?I?K?E?	
NP-2	401	G?K?N?H?K? - V? - F?Q?A?N? - N?D?A?T?E?V?V?L?N? - - - K?L?H?A?P?L?L?T?R?F?V?R?I?R?P?Q?T?W?H?S?G?I?A?R?	450
NP-1		G? - N? - K?P?V?L?F?Q?G?N?H?P? - T?D?V?V?V?A?V?P?K? - - - P?L?I?T?R?F?V?R?I?K?P?A?T?W?E?T?G?I?S?M?R?	
NP-2	451	L?E?L?F?C?R?V?T?D?A?P?C?S?H?M?L?G?M?L?G?M?L?G?M?L?G?M?L?G?M?V?S?G?L?I?A?D?S?Q?I?S?A?S?S?T?Q?E?Y?L? - W?S?P?S?A?R?L?V?S?	500
NP-1		F?E?V?Y?G?C?K?I?D?Y?P?C?S?G?M?L?G?M?V?S?G?L?I?S?D?S?Q?I? - S?S?N?Q?G?D?R?Y?W?N?P?E?N?I?R?V?T?S?	
NP-2	501	R?S?G?W?F? - P?R?P?Q?A?Q?P?G?E? - - - E?W?L?Q?V?D?L?G?T?P?K?T?V?K?G?V?I?I?Q?G?A?R?G?G?D?S?I?T?A?V?E?	550
NP-1		R?S?G?W?A?L?P? - - - P? - A? - P?H?S?Y?I?N?E?W?L?Q?I?D?L?G?E?E?K?I?V?R?G?I?I?I?Q?G? - - - G?K?H?R?E?N?K?V?	
NP-2	551	A?R?A?F?V?R?K?F?K?V?S?Y?S?L?N?G?K?D?W?E?Y?I?Q?D?P? - - - R?T?Q?Q?P?R?L?F?E?G?N?M?H?Y?D?T?P?D?I?R?R?E?D?	600
NP-1		- - - F?M?R?K?E?K?I?G?Y?S?N?H?G?S?D?W?K?M?I?D?D?S?K?R?K?A? - - - K?S?F?E?G?N?M?H?Y?D?T?P?E?I?R?T?F?	
NP-2	601	P?I?P?A?Q?Y?V?R?V? - - - Y?P?E?R?W?S?P?A? - - - G?I? - G?M?R?L?E?V?L?G?C?D?W?T?D?S?K?P?T?V?E? - - - T?L?G?P?	650
NP-1		P? - - A?L?S?T?R?F?I?R?I?Y?P?E? - - - A?T?H?G?G?L?G?L?R?M?E?L?L?G?C?E? - - - - - V?E?A?P?T?A?G?P?	
NP-2	651	T?V?K?S?E?E?T?T?P?Y?P?T?E?E?A?T?E?C?G?E? - - - N?C? - S?F?E? - D?D?K?D?L?Q? - - - L? - - - P?	700
NP-1		T? - - - T? - - - P?N?G?N?L?V?D? - - - E?C?D?D?D?Q?A?N?C?H?S?G?T?G?D?D?F?Q?L?T?G?G?T?T?V?L?A?T?E?K?P?	
NP-2	701	- - - S? - - - - - G?F?N?C?I?E?F? - - - - - F?L?E?E?P?C?G?W?M?Y?D? - H?A? - - K?W? - - L?R?T?T?	750
NP-1		V?I?D?S?T?I?Q?S?E?F?P?T?Y?G?N?C?E?F?G?W?G?S?H?K?T?F? - - - C?H?E?H?D?H?N?H?V?Q?L?K?W?S?V?L? - T?	
NP-2	751	W?A?S?S?S?2?N? - D?R?T?P?D?D?R?N?P?L?R?L?Q?S?D?S? - Q?E?G?Q?Y?A?R?L?I?S?P?P?V?H?L?P?R?S?P?V?C?H?	800
NP-1		- - - S?K?T?G?P?I?Q?D?H?T?G? - D?G? - N?F?I?Y?S?Q?A?D?E?N?Q?K? - G?K?V?A?R?L?V?S?P?V?V?Y?S?Q?N?S?A?H?C?M?	
NP-2	801	E?F?Q?Y?Q?A?T?G? - - - G? - - R?G?V?A?L? - - Q?V?V?R?E?A?S?Q?E?S?K?L?L?W?V? - I?R?E?D?Q?G?G?E?W?K?H?G?R?	850
NP-1		T?F?W?Y?H?M?S?G?H?V?G?T?L?R? - V?K?L?R?Y?Q?K?P?E?Y?D?Q? - - - L?V?W?M?A?I?G? - Q?G?D?H?W?K?E?G?R?	
NP-2	851	I?I?L?P? - S?Y?D?M?E?Y?Q? - I?V?F?E?G?V?I?G?K?G?R?S?G?E?I?A?D?D?I?R?I? - - - S?T?D?V?P?L?E?N?C?M?E?	900
NP-1		V?L?L?H?K?S?L?K?L? - Y?Q?V?I? - F?E?G?E?I?G?K?H?L?G?G?I?A?V?D?D?I?S?I?N?H?I?S?Q? - - - E?D?C?A?K?	
NP-2	901	P?I?S?A?F?A?G?E?N?F?R?D?I?P?E?I?H?E?R?E? - G? - - - Y?E?D?E?I?D?E?Y?E?V?D?W?S?N?S?S?A?T?S?G?S?	950
NP-1		P? - - A?D?D?L?K? - - - K?N? - - - P?E?I?K?I?D?E?T?G?S?T?P?G?Y?E?G?E?G? - - E?G? - - D?K? - N?I?S?R?K?P? - G?N?	
NP-2	951	G?A?P?S?D?K?E?K?S?W?I?Y?T?D?P?I?L?I?T?I?I?A?M?S?S?L?G?V?L?L?G?A?T?C?A?G?L?L?L?Y?C?T?C?S?V?G?L?	1000
NP-1		V?L? - - - K? - - - - - T?D?P?I?L?I?I?I?A?M?S?A?G?V?L?L?G?A?V?C? - G?V?V?Y?C?A?C?W?H?N?G?M?	
NP-2	1001	S?S?R? - - S?C?T?L?E?N?Y?N?F?E?L?Y?D?G? - - L?K?H?K?V?R?M?H?Q?C?C?S?E?A?	1038
NP-1		S?E?R?N?I?S?A? - - L?E?N?Y?N?F?E?L?V?D?G?V?K?L?K? - K?D?R?L?N?T?Q?S?T?Y?S?E?R?I?	

Figure 5

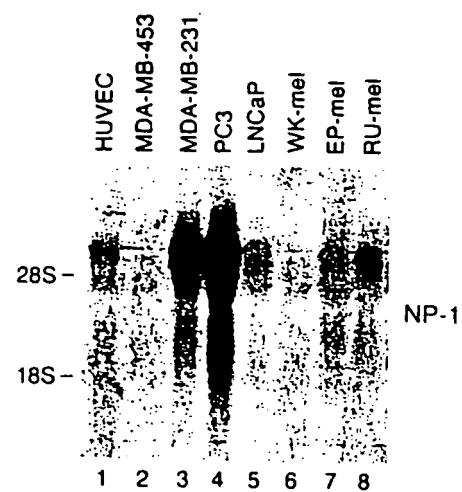


Figure 6

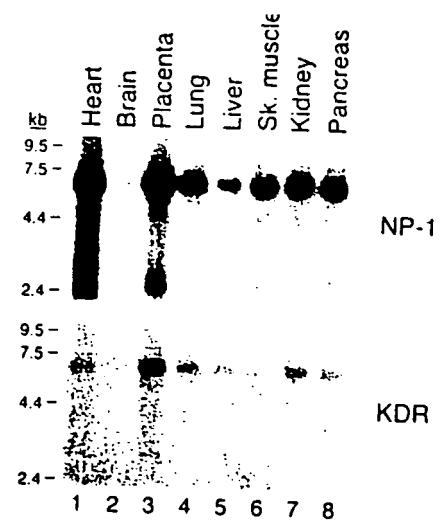


Figure 7A

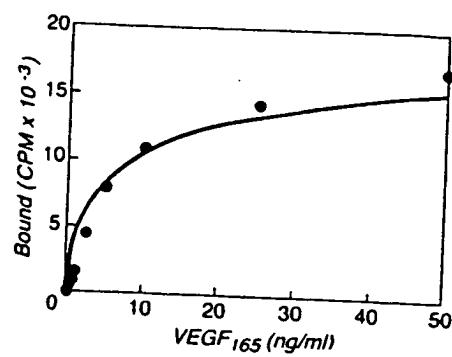


Figure 7B

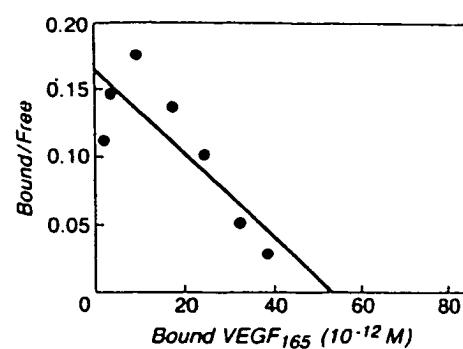


Figure 8

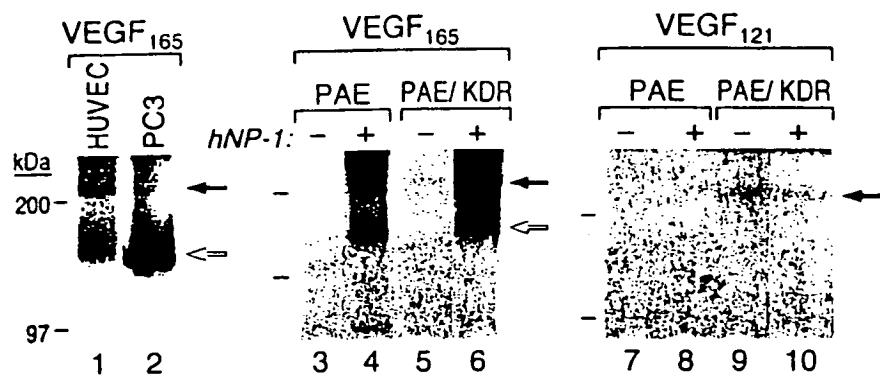


Figure 9

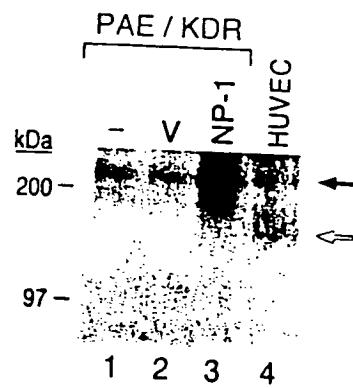


Figure 10

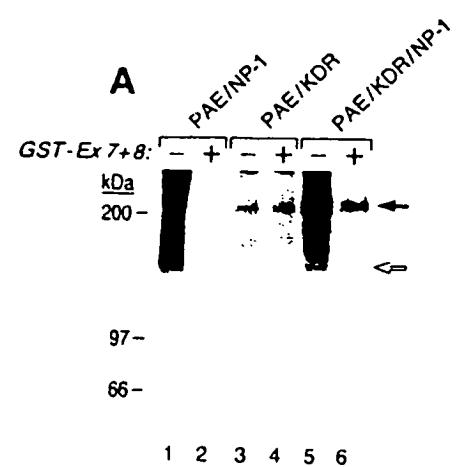


Figure 11A

KDR alone

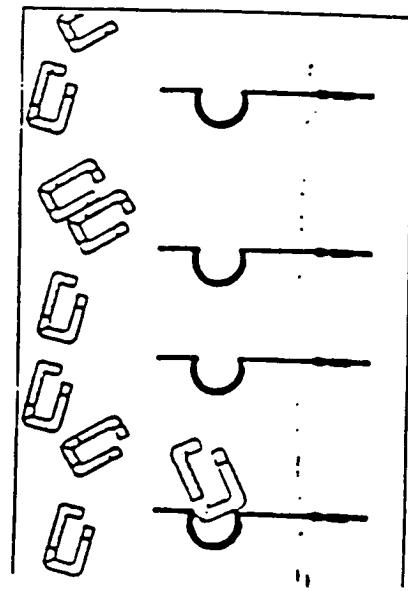
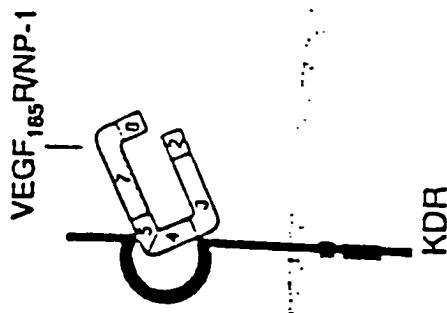


Figure 11B

KDR + VEGF<sub>165</sub>R/NP-1

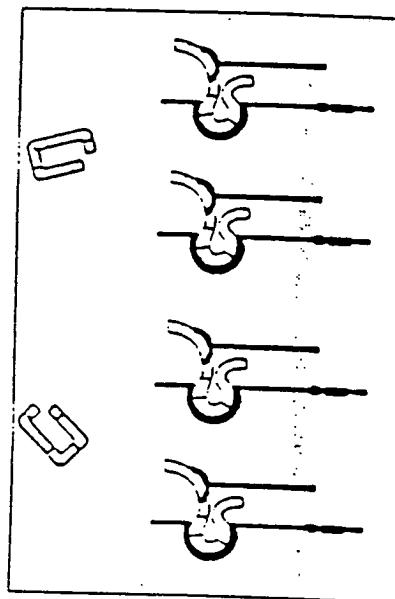
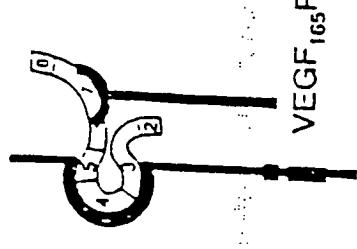


Figure 11C

KDR + VEGF<sub>165</sub>R/NP-1  
+ Exon 7

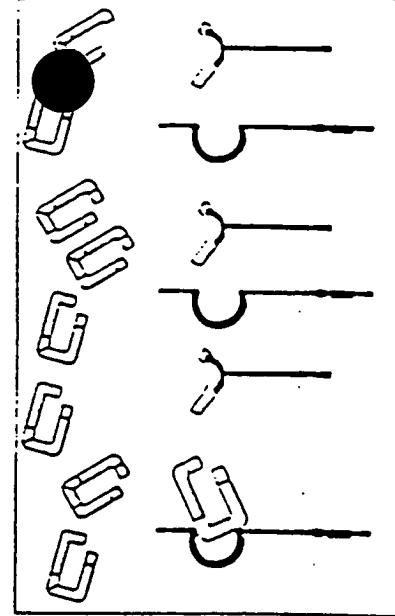
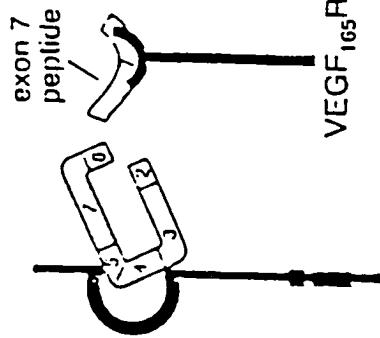


Figure 12

Human Neuropilin-2 amino acid sequence:

MCMFFLTWVFLALYFSRHQVRGQPDPPCGGRLNSKDAGYITSPGYPQDYPHSQN  
CEWIVYAPEPNQKIVLNFnNPHFEIEKHDCKYDFIEIRDGSESADLLGKHCGNIAPP  
TIISSGSMLYIKFTSDYARQGAGFSLRYEIFKTGSEDCSKNFTSPNGTIESPGFPEK  
YPHNLDCTFTILAKPKMEIILQFLIFDLEHDPLQVGEGDCKYDWLDIWDGIPHVGPL  
IGKYCGTKTPSELRSSTGILSLTFHTDMAVAKDGFSARYYLVHQELENFQCNVP  
LGMEGRRIANEQISASSTYSDGRWTPQGSRLHGDDNGWTFNLDNKEYLQVDLA  
FLTMLTIAITCGAISRETQNGYYVKSYKLEVSTNGEDWMVYRHGKNHKVFOANN  
DATEWLNKLHAPLLTRFVRIRPQTWHSGIALRLELFGCRVTDAPCSNMLGMILS  
GLIADSQISASSTQEYLWSPSAARLVSSASGWFPRIPOAQPGEEWLQVDLGTPK  
TVKGVIQGARGGDSITAVEARAFVRKFKVSYSLNGKDWEYIQDPRTQQPKLFEG  
NMHYDTPDIRRFDPPIAQYVRYVPERWSPAGIGMRLEVLGCDWTDSPKPTVETLG  
PTVKSEETTPYPTEEEATECGENCSFEDDKDLQLPSGFNCNDFLEEPGWMYD  
HAKWLATTWASSSSPNDRTFPDDRNFLRLQSDSQREGQYARLISPPVHLPRSPV  
CMEFQYQATGGRGVALQWREASQESKLLWIREDQGGEWKHGRIILPSYDMEYQ  
IVFEGVIGKGRSGEIAADDIRISTDVPLENCMEPISAFAGENFKVDIPEIHEREGYED  
EIDDEYEVDWSNSSSATSGSGAPSTDKEKSWLYTLDPILITIAMSSLGVLLGAT  
CAGLLLYCTCSYSGLSSRSCTTLENYNFELYDGLKHKVKMNHQKCCSEA\*

Figure 13

gaattcggca	cgagggaaa	ataaaagaga	aaaaaacaca	aagattaaa	caagaaacct	60
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aagagcgaag	agacaaccac	cccctacccc	accgaagagg	aggccacaga	gtgtgggag	1980
aactcgact	ttgaggatga	caaagattt	cagctccctt	cgggatttca	ttcaacttc	2040
gatttctcg	aggagccctg	tggttgatg	tatgtaccat	ccaaagtggct	ccggaccacc	2100
tggccagca	gttccagccc	aaacgaccgg	acgtttccag	atgacagaa	tttcttgggg	2160
ctgcagagt	acagccagag	agagggccag	tatgtccggc	tcatcagccc	ccctgtccac	2220
ctgccccgaa	gcccgggtgt	catggatcc	cagtaccagg	ccacggccgg	ccgggggtg	2280
gcgcgtcgagg	ttgtgcggga	agccaggccag	gagagcaagt	tgctgtgggt	catccgtgag	2340
gaccaggcg	gcgagtgaa	gcacggccgg	atcatcttc	ccagctacga	catggagtac	2400
cagattgtgt	tgcaggaggt	gatagggaaa	ggacgttcc	gagagattgc	cattgtatgc	2460
attcggataa	gcactgtatgt	cccactggag	aactgcatgg	aaccatctc	ggcttttgc	2520
ggtgagaatt	ttaaaatgtt	catcccagaa	atacatgaga	gagaaggata	tgaagatgaa	2580
attgtatgt	aatacgaggt	ggactggagc	aatttttctt	ctgcaaccc	agggtctggc	2640
gccccctcga	ccgacaaaaga	aaagagctgg	ctgtacaccc	tggatccat	cctcatcacc	2700
atcatcgcc	tgcgttact	gggcgttcc	ctgggggcca	cctgtgcagg	cctccgtctc	2760
tactgcaccc	gttccctactc	gggcgttgc	tcccgaaat	gcaccacact	ggagaactac	2820
aacttcgagc	tctacgttgc	ccttaagcac	aagtcaga	tgaaccacca	aaagtgtctc	2880
tccgaggcat	gacggattgc	acctgaatcc	tatctgacgt	ttcattcc	caagaggggc	2940
tggggaaat	tacattttt	tttcttttgc	aaactgaatg	ccataatctc	gatcaaaccg	3000
atccagaata	ccgaaggat	ggacaggaca	gaaaagcgag	tcgcaggagg	aaggagatg	3060
cagccgcaca	ggggatgtt	accctcttag	gaccgcgg	gctaagtcat	tgcaggaacg	3120
gggctgtgtt	ctctgtgttt	acaaaacagg	agctcatctc	tttggggtca	cagttctatt	3180
ttgtttgtt	gtttgttatt	tttattttat	atattttat	tctttgtt	gtggagcagt	3240
gtgagcaact	caaagaggca	gaagaggaga	atgactttt	cagaatagaa	gtggagcagt	3300
gatcatttatt	ctccgccttc	tctttctaat	caacacttga	aaagcaaaat	gtcttttcag	3360
cctttccatc	tttacaaata	aaactcaaaa	aagctgttca	gctt		3404

247 256 265 274 283 292  
 5' ATG GAG AGG GGG CTG CCG CTC CTC TGC GCC GTG CTC GCC CTC GTC CTC GCC CCG  
 M E R G L P L L C A V I A L V L A P  
 301 310 319 328 337 346  
 GCC GGC GCT TTT CGC AAC GAT AAA TGT GGC GAT ACT ATA AAA ATT GAA AGC CCC  
 A G A F R N D K C G D T I K I E S P  
 355 364 373 382 391 400  
 GGG TAC CTI ACA TCT CCT GGT TAT CCT CAT TCT TAT CAC CCA AGT GAA AAA TGC  
 G Y I T S P G Y P H S Y H P S E K C  
 409 418 427 436 445 454  
 GAA TGG CTG ATT CAG GCT CCG GAC CCA TAC CAG AGA ATT ATG ATC AAC TTC AAC  
 E W L I Q A P D P Y Q R I M I N F N  
 463 472 481 490 499 508  
 CCT CAC TTC GAT TTG GAG GAC AGA GAC TGC AAG TAT GAC TAC GTG GAA GTG TTC  
 P H F D L E D R D C K Y D Y V C V F  
 517 526 535 544 553 562  
 GAT GGA GAA AAT GAA AAT GGA CAT TTT AGG GGA AAG TTC TGT GGA AAG ATA GCC  
 D G E N E N G H F R G K F C G K I A  
 571 580 589 598 607 616  
 CCT CCT GTT GTG TCT TCA GGG CCA TTT CTT TTT ATC AAA TTT GTC TCT GAC  
 P P P V V S S G P F L F I K F V S D  
 625 634 643 652 661 670  
 TAC GAA ACA CAT GGT GCA GGA TTT TCC A1A CGT TAT GAA ATT T1C AAG AGA GGT  
 Y C T H G A G F S I R Y E I F K R G  
 679 688 697 706 715 724  
 CCT GAA TGT TCC CAG AAC TAC ACA ACA CCT AGT GGA GTG ATA AAG TCC CCC GGA  
 P E C S Q N Y T T P S G V I K S P G  
 a1 F C S Q N Y T T P S G V I K S P G  
 733 742 751 760 769 778  
 TTC CCT GAA AAA TAT CCC AAC AGC CTT GAA TGC ACT TAT ATT GTC TTT GCG CCA  
 F P E K Y P N S L E C T Y I V F A P  
 787 796 805 814 823 832  
 AAG ATG TCA GAG ATT ATC CTG GAA TTT GAA AGC TTT GAC CTG GAG CCT GAC TCA  
 K M S E I I L E F E S F D L E P D S  
 841 850 859 868 877 886  
 AAT CCT CCA GGG GGG ATG TTC TGT CGC TAC GAC CGG CTA GAA ATC TGG GAT GGA  
 N P P G G M F C R Y D R L F I W D G  
 895 904 913 922 931 940  
 TTC CCT GAT G11 GGC CCT CAC ATT GGG CGT TAC TGT GGA CAG AAA ACA CCA GGT  
 F P D V G P H I G R Y C G Q K T P G  
 949 958 967 976 985 994  
 CGA ATC CGA TCC TCA TCG GGC ATT C1C TCC ATG GTT TTT TAC ACC GAC AGC GCG  
 R I R S S S G I L S M V F Y T D S A

1003 1012 1021 1030 1039 1048  
 ATA GCA AAA GAA GGT TTC TCA GCA AAC TAC AGT GTC TTG CAG AGC AGC TCA  
 I A K E G F S A N Y S V L Q S S V S  
  
 1057 1066 1075 1084 1093 1102  
 GAA GAA TTC AAA TGT ATG GAA GCT CTG GGC ATG GAA TCA GGA GAA ATT CAT TCT  
 E D F K C M C A L G M E S G E I H S  
 61 61  
  
 1111 1120 1129 1138 1147 1156  
 GAC CAG ATC ACA GCT TCT TCC CAG TAT AGC ACC AAC TGG TCT GCA GAG CGC TCC  
 D Q I T A S S Q Y S T N W S A E R S  
  
 1165 1174 1183 1192 1201 1210  
 CGC CTG AAC TAC CCT GAG AAT GGG TGG ACT CCC GGA GAG GAT TCC TAC CGA GAG  
 R L N Y P E N G W T P G E D S Y R E  
  
 1219 1228 1237 1246 1255 1264  
 TGG ATA CAG GTA GAC TTG GGC CTT CTG CGC TTT GTC ACG GCT GTC GGG ACA CAG  
 W I Q V D L G L L R F V T A V G T Q  
  
 1273 1282 1291 1300 1309 1318  
 GGC GCC ATT TCA AAA GAA ACC AAG AAG AAA TAT TAT GTC AAG ACT TAC AAG ATC  
 G A I S K E T K K Y Y V K T Y K I  
  
 1327 1336 1345 1354 1363 1372  
 GAC GTT AGC TCC AAC GGG GAA GAC TGG ATC ACC ATA AAA GAA GGA AAC AAA CCT  
 D V S S N G E D W I T I K E G N K P  
  
 1381 1390 1399 1408 1417 1426  
 GAT CTC TTT CAG GGA AAC ACC AAC CCC ACA GAT GTT GTG GTT GCA GTA TTC CCC  
 V L F Q G N T N P T O V V V A V F P  
  
 1435 1444 1453 1462 1471 1480  
 AAA CCA CTG ATA ACT CGA TTT GTC CGA ATC AAG CCT GCA ACT TGG GAA ACT GGC  
 K P L I T R F V R I K P A T W E T G  
  
 1489 1498 1507 1516 1525 1534  
 ATA TCA ATG AGA TTT GAA GTA TAC GGT TGC AAG ATA ACA GAT TAA CCT TGC TCT  
 I S M R F E V Y G C K I T D Y 61 C 62 S  
  
 1543 1552 1561 1570 1579 1588  
 GGA ATG TTG GGT ATG GTG TCT GGA CTT ATT TCT GAC TCC CAG ATC ACA TCA TCC  
 G M L G M V S G L I S D S Q I T S S  
  
 1597 1606 1615 1624 1633 1642  
 AAC CAA GGG GAC AGA AAC TGG ATG CCT GAA AAC ATC CGC CTG GTA ACC AGT CGC  
 N Q G D R N W M P E N I R L V T S R  
  
 1651 1660 1669 1678 1687 1696  
 TCT GGC TGG GCA CTT CCA CCC GCA CCT CAT TCC TAC ATC AAT GAG TGG CTC CAA  
 S G W A L P P A P H S Y I N E W L Q  
  
 1705 1714 1723 1732 1741 1750  
 ATA GAC CTG GGG GAG GAG AAG ATC GTG AGG GGC ATC ATC ATT CAG GGT GGG AAG  
 I D L G E E K I V R G I I I Q G G K  
  
 1759 1768 1777 1786 1795 1804  
 CAC CGA GAG AAC AAG GTG TTC ATG AGG AAG TTC AAG ATC GGG TAC AGC AAC AAC  
 H R E N K V F M R K F K I G Y S N N

1813 1814 1831 1840 1841 1858  
GGC TCG GAC TGG AAG ATG ATC ATG GAT GAC AGC AAA CGC AAG GCG TGT TCT TTT

G S D W K M I M D D S K R K A K S F

1867 1876 1885 1894 1903 1912  
GAG GGC AAC AAC AAC TAT GAT ACA CCT GAG CTG CGG ACT TTT CCA GCT CTC TCC

E G N N N Y D T P E L R T F P A L S

1921 1930 1939 1948 1957 1966  
ACG CGA TTC ATC AGG ATC TAC CCC GAG AGA GCC ACT CAT GGC GGA CTG GGG CTC

T R F I R I Y P F R A T H G G L G L

1975 1984 1993 2002 2011 2020  
AGA ATG GAG CTG CTG GGC TGT GAA GTG GAA GCC CCT ACA GCT GGA CCG ACC ACT

R M E L L G C E V b d A P T A G P T T

2029 2038 2047 2056 2065 2074  
CCC AAC GGG AAC TTG GTG GAT GAA TGT GAT GAC GAC CAG GCC AAC TGC CAC AGT

P N G N L V D E C D D D Q A N C H S

2083 2092 2101 2110 2119 2128  
GGA ACA GGT GAT GAC TTC CAG CTC ACA GGT GGC ACC ACT GTG CTG GCC ACA GAA

G T G D D F Q L T G G T T V L A T E

2137 2146 2155 2164 2173 2182  
AAG CCC ACG GTC ATA GAC AGC ACC ATA CAA TCA GAG TTT CCA ACA TAT GGT TTT

K P T V I D S T I Q S E F P T Y L G C

2191 2200 2209 2218 2227 2236  
AAC TGT GAA TTT GGC TGG GGC TCT CAC AAG ACC TTC TGC CAC TGG GAA CAT GAC

N C E F G W G S H K T F C H W E H D

2245 2254 2263 2272 2281 2290  
AAT CAC GTG CAG CTC AAG TGG AGT GTG TTG ACC AGC AAG ACG GGA CCC ATT CAG

N H V Q L K W S V L T S K T G P I O

2299 2308 2317 2326 2335 2344  
GAT CAC ACA GGA GAT GGC AAC TTC ATC TAT TCC CAA GCT GAC GAA AAT CAG AAG

D H T G D G N F I Y S Q A D E N Q K

2353 2362 2371 2380 2389 2398  
GGC AAA GTG GCT CGC CTG GTG AGC CCT GTG GTT TAT TCC CAG AAC TCT GCC CAC

G K V A R L V S P V V Y S Q N S A H

2407 2416 2425 2434 2443 2452  
TGC ATG ACC TTC TGG TAT CAC ATG TCT GGG TCC CAC GTC GGC ACA CTC AGG GTC

C M T F W Y H M S G S H V G T L R V

2461 2470 2479 2488 2497 2506  
AAA CTG CGC TAC CAG AAG CCA GAG GAG TAC GAT CAG CTC GTC TGG ATG GCC ATT

K L R Y Q K P E E Y D Q L V W M A I

2515 2524 2533 2542 2551 2560  
GGA CAC CAA GGT GAC CAC TGG AAG GAA GGG CGT GTC TTG CTC CAC AAG TCT CTG

G H Q G D H W K E G R V L L H K S L

2569 2578 2587 2596 2605 2614  
AAA CTT TAT CAG GTG ATT TTC GAG GGC GAA ATC GGA AAA GGA AAC CTT GGT GGG II

K L Y Q V T F E G E I G K G N L G G

Figure 14D

2623 263 2641 2650 2659 2668  
 ATT GCT GTG GAT GAC ATT AGT ATT AAC AAC CAC ATT TCA CAA GAA TGT GCA  
 I A V D D T S I N N H I S Q E D C A

2677 2686 2695 2704 2713 2722  
 AAA CCA GCA GAC CTG GAT AAA AAG AAC CCA GAA ATT AAA ATT GAT GAA ACA GGG  
 K P A D L D K K N P E I K I D F T G

2731 2740 2749 2758 2767 2776  
 AGC ACG CCA GGA TAC GAA GGT GAA GGA GAA GGT GAC AAG AAC ATC TCC AGG AAG  
 S T P G Y E G E G E G D K N I S R K

2785 2794 2803 2812 2821 2830  
 CCA GGC AAT GTG TTG AAG ACC TTA GAT CCC ATC CTC ATC ACC ATC ATA GCC ATG  
 P G N V L K T L D P L I T M I T I I A M

2839 2848 2857 2866 2875 2884  
 AGT GCC CTG GGG GTC CTC CTG GGG GCT GTC TGT GGG GTC GTG CTG TAC TGT GCC  
 S A L G V L L G A V C G V V L Y C A

2893 2902 2911 2920 2929 2938  
 TGT TGG CAT AAT GGG ATG TCA GAA AGA AAC TTG TCT GCC C'G GAG AAC TAT AAC  
 C M W L I N G M S E R N L S A L E N Y N

2947 2956 2965 2974 2983 2997  
 TTT GAA CTT GTG GAT GGT GTG AAG TTG AAA AAA GAC AAA CTG AAT ACA CAG AGT  
 F R L V D G V K L K X D K L N T Q S

3001 3010  
 ACT TAT TCG GAG GCA TGA 3' (SEQ ID NO: 1)  
 T Y S E A (SEQ ID NO: 4)  
 cyto 2

Figure 15A

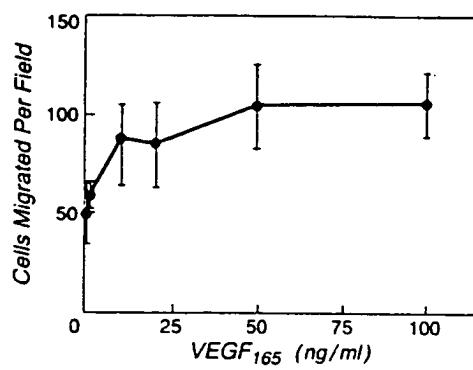


Figure 15B

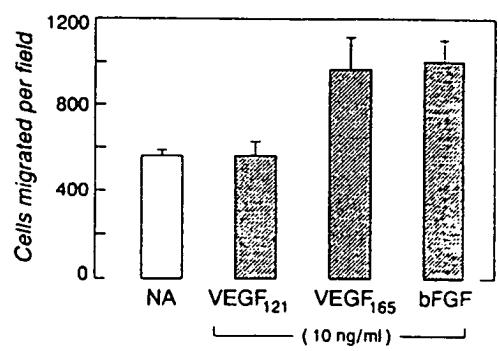


Figure 16A

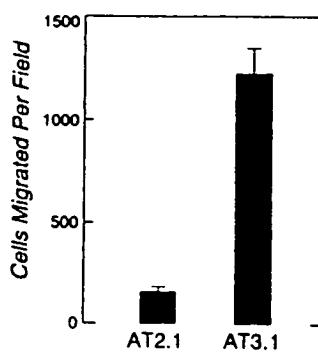


Figure 16B

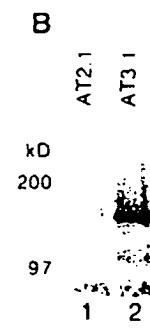


Figure 16C

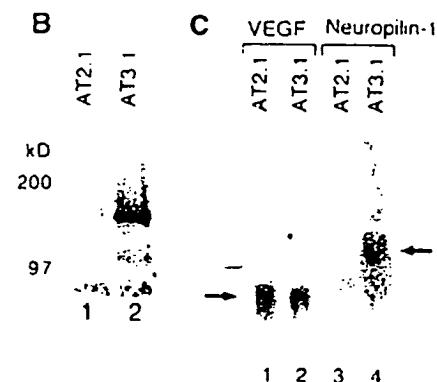


Figure 17A

Figure 17B

Figure 17C

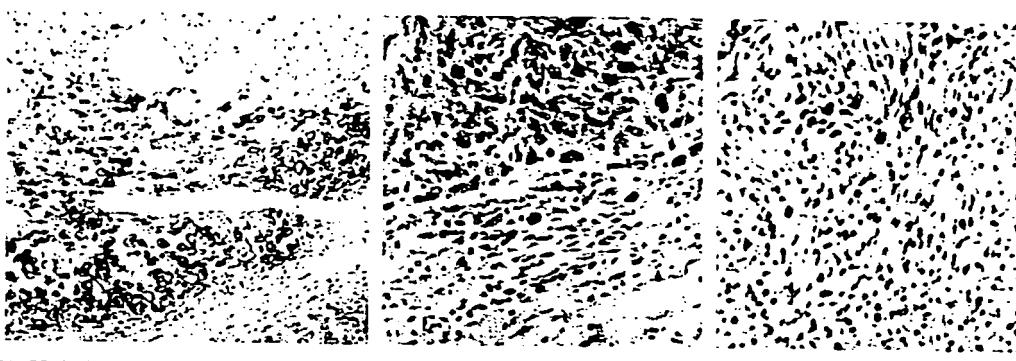


Figure 18A

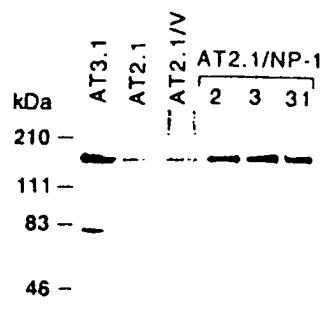
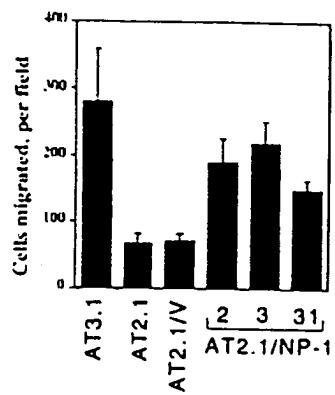


Figure 18B



$\beta$ -actin

NP-2

NP-1

RU  
EP  
WK  
PC3  
LNCaP  
231  
U87  
T47  
SK  
Jurkat  
HUVEC  
RPE

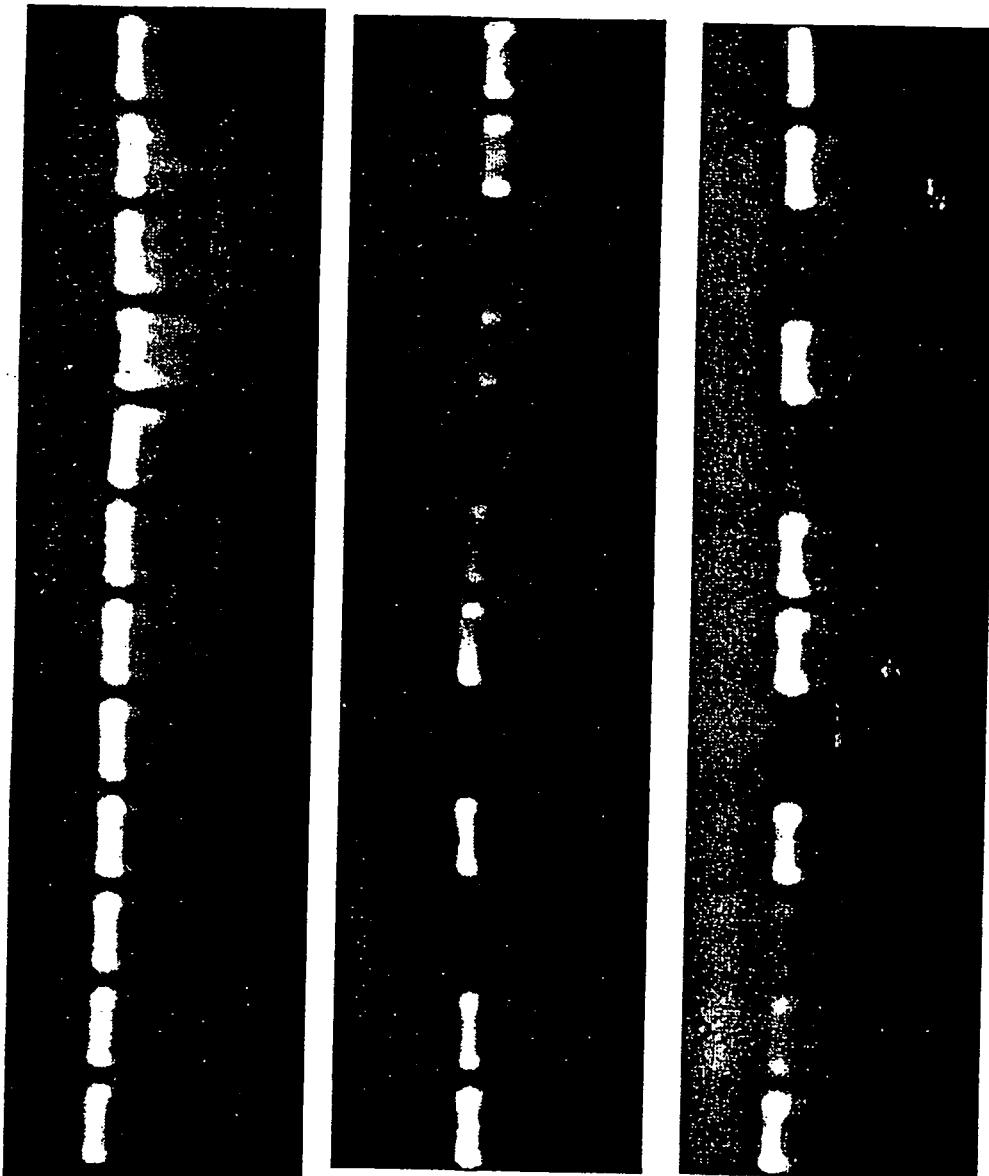


Figure 2a

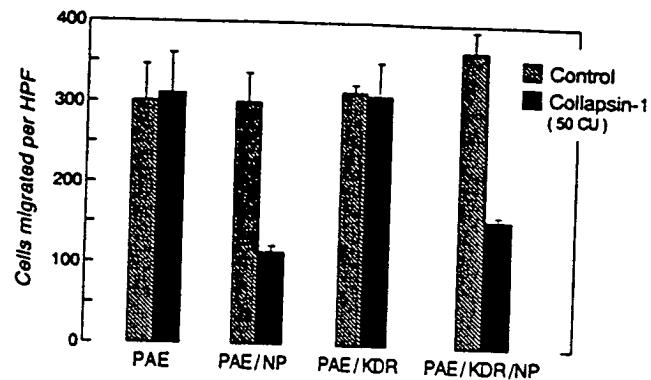


Figure 21A

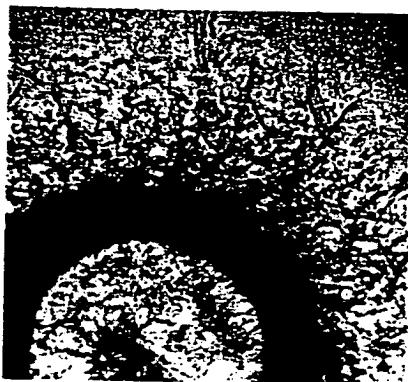


Figure 21B

